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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/025,524

DATE: 07/24/2002

TIME: 09:06:41

Input Set : A:\EP.txt

Output Set: N:\CRF3\07242002\J025524.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Gallatin, W. Michael
6 Kilgannon, Patrick D.
8 (ii) TITLE OF INVENTION: ICAM-4 Materials and Methods
10 (iii) NUMBER OF SEQUENCES: 42
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
14 (B) STREET: 233 South Wacker Drive, 6300 Sears Tower
15 (C) CITY: Chicago
16 (D) STATE: Illinois
17 (E) COUNTRY: United States of America
18 (F) ZIP: 60606-6402
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
26 (vi) CURRENT APPLICATION DATA:
C--> 27 (A) APPLICATION NUMBER: US/10/025,524
C--> 28 (B) FILING DATE: 18-Dec-2001
29 (C) CLASSIFICATION:
55 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: US 07/827,689
33 (B) FILING DATE: 27-JAN-1992
36 (A) APPLICATION NUMBER: US 07/889,724
37 (B) FILING DATE: 26-MAY-1992
40 (A) APPLICATION NUMBER: US 07/894,061
41 (B) FILING DATE: 05-JUN-1992
44 (A) APPLICATION NUMBER: US 08/009,266
45 (B) FILING DATE: 22-JAN-1993
48 (A) APPLICATION NUMBER: US 08/102,852
49 (B) FILING DATE: 05-AUG-1993
52 (A) APPLICATION NUMBER: US 08/245,295
53 (B) FILING DATE: 18-MAY-1994
56 (A) APPLICATION NUMBER: US 08/485,604
57 (B) FILING DATE: 07-JUN-1995
59 (viii) ATTORNEY/AGENT INFORMATION:
60 (A) NAME: WILLIAMS, JR. JOSEPH A.
61 (B) REGISTRATION NUMBER: 38,659
62 (C) REFERENCE/DOCKET NUMBER: 27866/33321
64 (ix) TELECOMMUNICATION INFORMATION:
65 (A) TELEPHONE: 312-474-6300

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66          (B) TELEFAX: 312-474-0448
67          (C) TELEX: 25-3856
69 (2) INFORMATION FOR SEQ ID NO: 1:
71   (i) SEQUENCE CHARACTERISTICS:
72       (A) LENGTH: 2988 base pairs
73       (B) TYPE: nucleic acid
74       (C) STRANDEDNESS: single
75       (D) TOPOLOGY: linear
77   (ii) MOLECULE TYPE: cDNA
80   (ix) FEATURE:
81       (A) NAME/KEY: CDS
82       (B) LOCATION: 61..2814
84   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
86 AATTCGATCA CTCGCGCTCC CCTCGCCTTC TGCCTCTCTCC CCTCCCTGGC AGCGGCGGCA      60
88 ATG CCG GGG CCT TCA CCA GGG CTG CGC CGA ACG CTC CTC GGC CTC TGG      108
89 Met Pro Gly Pro Ser Pro Gly Leu Arg Arg Thr Leu Leu Gly Leu Trp
90 1      5      10      15
92 GCT GCC CTG GGC CTG GGG ATC CTA GGC ATC TCA GCG GTC GCG CTA GAA      156
93 Ala Ala Leu Gly Leu Gly Ile Leu Gly Ile Ser Ala Val Ala Leu Glu
94      20      25      30
96 CCT TTC TGG GCG GAC CTT CAG CCC CGC GTG GCG CTC GTG GAG CGC GGG      204
97 Pro Phe Trp Ala Asp Leu Gln Pro Arg Val Ala Leu Val Glu Arg Gly
98      35      40      45
100 GGC TCG CTG TGG CTC AAC TGC AGC ACT AAC TGT CCG AGG CCG GAG CGC      252
101 Gly Ser Leu Trp Leu Asn Cys Ser Thr Asn Cys Pro Arg Pro Glu Arg
102      50      55      60
104 GGT GGC CTG GAG ACC TCG CTA CGC CGA AAC GGG ACC CAG AGG GGT CTG      300
105 Gly Gly Leu Glu Thr Ser Leu Arg Arg Asn Gly Thr Gln Arg Gly Leu
106 65      70      75      80
108 CGC TGG CTG GCT CGA CAG CTG GTG GAC ATC CGA GAG CCT GAA ACC CAG      348
109 Arg Trp Leu Ala Arg Gln Leu Val Asp Ile Arg Glu Pro Glu Thr Gln
110      85      90      95
112 CCG GTC TGC TTC TTC CGC TGC GCG CGC CGC ACA CTC CAA GCG CGT GGG      396
113 Pro Val Cys Phe Phe Arg Cys Ala Arg Arg Thr Leu Gln Ala Arg Gly
114      100      105      110
116 CTC ATC CGA ACT TTC CAG CGA CCG GAT CGG GTA GAG CTA GTG CCT CTG      444
117 Leu Ile Arg Thr Phe Gln Arg Pro Asp Arg Val Glu Leu Val Pro Leu
118      115      120      125
120 CCT CCT TGG CAG CCT GTA GGT GAG AAC TTC ACC TTG AGC TGC AGG GTC      492
121 Pro Pro Trp Gln Pro Val Gly Glu Asn Phe Thr Leu Ser Cys Arg Val
122      130      135      140
124 CCG GGG GCA GGA CCC CGA GCG AGC CTC ACA TTG ACC TTG CTG CGA GGC      540
125 Pro Gly Ala Gly Pro Arg Ala Ser Leu Thr Leu Thr Leu Leu Arg Gly
126 145      150      155      160
128 GGC CAG GAG CTG ATT CGC CGA AGT TTC GTA GGC GAG CCA CCC CGA GCT      588
129 Gly Gln Glu Leu Ile Arg Arg Ser Phe Val Gly Glu Pro Pro Arg Ala
130      165      170      175
132 CGG GGT GCG ATG CTC ACC GCC ACG GTC CTG GCG CGC AGA GAG GAT CAC      636
133 Arg Gly Ala Met Leu Thr Ala Thr Val Leu Ala Arg Arg Glu Asp His

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134	180	185	190	
136	AGG GCC AAT TTC TCA TGC CTC GCG GAG CTT GAC CTG CGG CCA CAC GGC	684		
137	Arg Ala Asn Phe Ser Cys Leu Ala Glu Leu Asp Leu Arg Pro His Gly			
138	195 200 205			
140	TTG GGA CTG TTT GCA AAC AGC TCA GCC CCC AGA CAG CTC CGC ACG TTT	732		
141	Leu Gly Leu Phe Ala Asn Ser Ser Ala Pro Arg Gln Leu Arg Thr Phe			
142	210 215 220			
144	GCC ATG CCT CCA CTT TCC CCG AGC CTT ATT GCC CCA CGA TTC TTA GAA	780		
145	Ala Met Pro Pro Leu Ser Pro Ser Leu Ile Ala Pro Arg Phe Leu Glu			
146	225 230 235 240			
148	GTG GGC TCA GAA AGG CCG GTG ACT TGC ACT TTG GAT GGA CTG TTT CCT	828		
149	Val Gly Ser Glu Arg Pro Val Thr Cys Thr Leu Asp Gly Leu Phe Pro			
150	245 250 255			
152	GCC CCA GAA GCC GGG GTT TAC CTC TCT CTG GGA GAT CAG AGG CTT CAT	876		
153	Ala Pro Glu Ala Gly Val Tyr Leu Ser Leu Gly Asp Gln Arg Leu His			
154	260 265 270			
156	CCT AAT GTG ACC CTC GAC GGG GAG AGC CTT GTG GCC ACT GCC ACA GCT	924		
157	Pro Asn Val Thr Leu Asp Gly Glu Ser Leu Val Ala Thr Ala Thr Ala			
158	275 280 285			
160	ACA GCA AGT GAA GAA CAG GAA GGC ACC AAA CAG CTG ATG TGC ATC GTG	972		
161	Thr Ala Ser Glu Glu Gln Glu Gly Thr Lys Gln Leu Met Cys Ile Val			
162	290 295 300			
164	ACC CTC GGG GGC GAA AGC AGG GAG ACC CAG GAA AAC CTG ACT GTC TAC	1020		
165	Thr Leu Gly Gly Glu Ser Arg Glu Thr Gln Glu Asn Leu Thr Val Tyr			
166	305 310 315 320			
168	AGC TTC CCG GCT CCT CTT CTG ACT TTA AGT GAG CCA GAA GCC CCC GAG	1068		
169	Ser Phe Pro Ala Pro Leu Leu Thr Leu Ser Glu Pro Glu Ala Pro Glu			
170	325 330 335			
172	GGA AAG ATG GTG ACC GTA AGC TGC TGG GCA GGG GCC CGA GCC CTT GTC	1116		
173	Gly Lys Met Val Thr Val Ser Cys Trp Ala Gly Ala Arg Ala Leu Val			
174	340 345 350			
176	ACC TTG GAG GGA ATT CCA GCT GCG GTC CCT GGG CAG CCC GCT GAG CTC	1164		
177	Thr Leu Glu Gly Ile Pro Ala Ala Val Pro Gly Gln Pro Ala Glu Leu			
178	355 360 365			
180	CAG TTA AAT GTC ACA AAG AAT GAC GAC AAG CGG GGC TTC TTC TGC GAC	1212		
181	Gln Leu Asn Val Thr Lys Asn Asp Asp Lys Arg Gly Phe Phe Cys Asp			
182	370 375 380			
184	GCT GCC CTC GAT GTG GAC GGG GAA ACT CTG AGA AAG AAC CAG AGC TCT	1260		
185	Ala Ala Leu Asp Val Asp Gly Glu Thr Leu Arg Lys Asn Gln Ser Ser			
186	385 390 395 400			
188	GAG CTT CGT GTT CTG TAC GCA CCT CGG CTG GAT GAC TTG GAC TGT CCC	1308		
189	Glu Leu Arg Val Leu Tyr Ala Pro Arg Leu Asp Asp Leu Asp Cys Pro			
190	405 410 415			
192	AGG AGC TGG ACG TGG CCA GAG GGT CCA GAG CAG ACC CTC CAC TGC GAG	1356		
193	Arg Ser Trp Thr Trp Pro Glu Gly Pro Glu Gln Thr Leu His Cys Glu			
194	420 425 430			
196	GCC CGT GGA AAC CCT GAG CCC TCC GTG CAC TGT GCA AGG CCT GAC GGT	1404		
197	Ala Arg Gly Asn Pro Glu Pro Ser Val His Cys Ala Arg Pro Asp Gly			
198	435 440 445			

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200	GGG	GCG	GTG	CTA	GCG	CTG	GGC	CTG	TTG	GGT	CCA	GTG	ACC	CGT	GCC	CTC	1452
201	Gly	Ala	Val	Leu	Ala	Leu	Gly	Leu	Leu	Gly	Pro	Val	Thr	Arg	Ala	Leu	
202		450					455					460					
204	GCG	GGC	ACT	TAC	CGA	TGT	ACA	GCA	ATC	AAT	GGG	CAA	GGC	CAG	GCG	GTC	1500
205	Ala	Gly	Thr	Tyr	Arg	Cys	Thr	Ala	Ile	Asn	Gly	Gln	Gly	Gln	Ala	Val	
206	465					470					475					480	
208	AAG	GAT	GTG	ACC	CTG	ACT	GTG	GAA	TAT	GCC	CCA	GCG	CTG	GAC	AGT	GTA	1548
209	Lys	Asp	Val	Thr	Leu	Thr	Val	Glu	Tyr	Ala	Pro	Ala	Leu	Asp	Ser	Val	
210					485					490					495		
212	GGC	TGC	CCA	GAA	CGT	ATT	ACT	TGG	CTG	GAG	GGG	ACA	GAG	GCA	TCG	CTT	1596
213	Gly	Cys	Pro	Glu	Arg	Ile	Thr	Trp	Leu	Glu	Gly	Thr	Glu	Ala	Ser	Leu	
214				500					505					510			
216	AGC	TGT	GTG	GCA	CAC	GGG	GTC	CCA	CCA	CCT	AGC	GTG	AGC	TGT	GTG	CGC	1644
217	Ser	Cys	Val	Ala	His	Gly	Val	Pro	Pro	Pro	Ser	Val	Ser	Cys	Val	Arg	
218			515					520						525			
220	TCT	GGA	AAG	GAG	GAA	GTC	ATG	GAA	GGG	CCC	CTG	CGT	GTG	GCC	CGG	GAG	1692
221	Ser	Gly	Lys	Glu	Glu	Val	Met	Glu	Gly	Pro	Leu	Arg	Val	Ala	Arg	Glu	
222		530				535						540					
224	CAC	GCT	GGC	ACT	TAC	CGA	TGC	GAA	GCC	ATC	AAC	GCC	AGG	GGA	TCA	GCG	1740
225	His	Ala	Gly	Thr	Tyr	Arg	Cys	Glu	Ala	Ile	Asn	Ala	Arg	Gly	Ser	Ala	
226	545					550					555					560	
228	GCC	AAA	AAT	GTG	GCT	GTC	ACG	GTG	GAA	TAT	GGT	CCC	AGT	TTT	GAG	GAG	1788
229	Ala	Lys	Asn	Val	Ala	Val	Thr	Val	Glu	Tyr	Gly	Pro	Ser	Phe	Glu	Glu	
230				565						570					575		
232	TTG	GGC	TGC	CCC	AGC	AAC	TGG	ACT	TGG	GTA	GAA	GGA	TCT	GGA	AAA	CTG	1836
233	Leu	Gly	Cys	Pro	Ser	Asn	Trp	Thr	Trp	Val	Glu	Gly	Ser	Gly	Lys	Leu	
234				580					585					590			
236	TTT	TCC	TGT	GAA	GTT	GAT	GGG	AAG	CCG	GAA	CCA	CGC	GTG	GAG	TGC	GTG	1884
237	Phe	Ser	Cys	Glu	Val	Asp	Gly	Lys	Pro	Glu	Pro	Arg	Val	Glu	Cys	Val	
238			595				600							605			
240	GGC	TCG	GAG	GGT	GCA	AGC	GAA	GGG	GTA	GTG	TTG	CCC	CTG	GTG	TCC	TCG	1932
241	Gly	Ser	Glu	Gly	Ala	Ser	Glu	Gly	Val	Val	Leu	Pro	Leu	Val	Ser	Ser	
242		610					615					620					
244	AAC	TCT	GGT	TCC	AGA	AAC	TCT	ATG	ACT	CCT	GGT	AAC	CTG	TCA	CCG	GGT	1980
245	Asn	Ser	Gly	Ser	Arg	Asn	Ser	Met	Thr	Pro	Gly	Asn	Leu	Ser	Pro	Gly	
246	625					630					635				640		
248	ATT	TAC	CTC	TGC	AAC	GCC	ACC	AAC	CGG	CAT	GGC	TCC	ACA	GTC	AAA	ACA	2028
249	Ile	Tyr	Leu	Cys	Asn	Ala	Thr	Asn	Arg	His	Gly	Ser	Thr	Val	Lys	Thr	
250					645					650					655		
252	GTC	GTC	GTG	AGC	GCG	GAA	TCA	CCG	CCA	CAG	ATG	GAT	GAA	TCC	AGT	TGC	2076
253	Val	Val	Val	Ser	Ala	Glu	Ser	Pro	Pro	Gln	Met	Asp	Glu	Ser	Ser	Cys	
254				660					665					670			
256	CCG	AGT	CAC	CAG	ACA	TGG	CTG	GAA	GGA	GCC	GAG	GCT	ACT	GCG	CTG	GCC	2124
257	Pro	Ser	His	Gln	Thr	Trp	Leu	Glu	Gly	Ala	Glu	Ala	Thr	Ala	Leu	Ala	
258			675						680					685			
260	TGC	AGT	GCC	AGA	GGC	CGC	CCC	TCT	CCA	CGC	GTG	CGC	TGT	TCC	AGG	GAA	2172
261	Cys	Ser	Ala	Arg	Gly	Arg	Pro	Ser	Pro	Arg	Val	Arg	Cys	Ser	Arg	Glu	
262		690					695					700					
264	GGT	GCA	GCC	AGG	CTG	GAG	AGG	CTA	CAG	GTG	TCC	CGA	GAG	GAT	GCG	GGG	2220

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265 Gly Ala Ala Arg Leu Glu Arg Leu Gln Val Ser Arg Glu Asp Ala Gly
266 705          710          715          720
268 ACC TAC CTG TGT GTG GCT ACC AAC GCG CAT GGC ACG GAT TCA CGG ACC      2268
269 Thr Tyr Leu Cys Val Ala Thr Asn Ala His Gly Thr Asp Ser Arg Thr
270          725          730          735
272 GTC ACT GTG GGT GTG GAA TAC CGG CCT GTG GTG GCT GAG CTG GCA GCC      2316
273 Val Thr Val Gly Val Glu Tyr Arg Pro Val Val Ala Glu Leu Ala Ala
274          740          745          750
276 TCG CCC CCA AGC GTG CGG CCT GGC GGA AAC TTC ACT CTG ACC TGC CGT      2364
277 Ser Pro Pro Ser Val Arg Pro Gly Gly Asn Phe Thr Leu Thr Cys Arg
278          755          760          765
280 GCA GAG GCC TGG CCT CCA GCC CAG ATC AGC TGG CGC GCG CCC CCG GGA      2412
281 Ala Glu Ala Trp Pro Pro Ala Gln Ile Ser Trp Arg Ala Pro Pro Gly
282          770          775          780
284 GCT CTC AAC CTC GGT CTC TCC AGC AAC AAC AGC ACG CTG AGC GTG GCG      2460
285 Ala Leu Asn Leu Gly Leu Ser Ser Asn Asn Ser Thr Leu Ser Val Ala
286 785          790          795          800
288 GGT GCC ATG GGC AGC CAT GGT GGC GAG TAT GAG TGC GCA GCC ACC AAT      2508
289 Gly Ala Met Gly Ser His Gly Gly Glu Tyr Glu Cys Ala Ala Thr Asn
290          805          810          815
292 GCG CAT GGG CGC CAC GCA CGG CGC ATC ACG GTG CGC GTG GCC GGT CCA      2556
293 Ala His Gly Arg His Ala Arg Arg Ile Thr Val Arg Val Ala Gly Pro
294          820          825          830
296 TGG CTG TGG GTC GCT GTG GGC GGT GCG GCA GGG GGC GCG GCG CTG CTG      2604
297 Trp Leu Trp Val Ala Val Gly Gly Ala Ala Gly Gly Ala Ala Leu Leu
298          835          840          845
300 GCC GCA GGG GCC GGC CTG GCC TTC TAC GTG CAG TCC ACC GCT TGC AAG      2652
301 Ala Ala Gly Ala Gly Leu Ala Phe Tyr Val Gln Ser Thr Ala Cys Lys
302          850          855          860
304 AAG GGA GAG TAC AAC GTC CAG GAG GCT GAG AGC TCA GGC GAG GCG GTG      2700
305 Lys Gly Glu Tyr Asn Val Gln Glu Ala Glu Ser Ser Gly Glu Ala Val
306 865          870          875          880
308 TGT CTC AAT GGC GCG GGC GGG ACA CCG GGT GCA GAA GGC GGA GCA GAG      2748
309 Cys Leu Asn Gly Ala Gly Gly Thr Pro Gly Ala Glu Gly Gly Ala Glu
310          885          890          895
312 ACC CCC GGC ACT GCC GAG TCA CCT GCA GAT GGC GAG GTT TTC GCC ATC      2796
313 Thr Pro Gly Thr Ala Glu Ser Pro Ala Asp Gly Glu Val Phe Ala Ile
314          900          905          910
316 CAG CTG ACA TCT TCC TGAGCCTGTA TCCAGCTCCC CCAGGGGCCT CGAAAGCACA      2851
317 Gln Leu Thr Ser Ser
318          915
320 GGGGTGGACG TATGTATTGT TCACTCTCTA TTTATTCAAC TCCAGGGGCG TCGTCCCCGT      2911
322 TTTCTACCCA TTCCCTTAAT AAAGTTTTTA TAGGAGAAAA AAAAAAAAAA AAAAAAAAAA      2971
324 AAAAAAAAAA AAAAAA      2988
326 (2) INFORMATION FOR SEQ ID NO: 2:
328     (i) SEQUENCE CHARACTERISTICS:
329         (A) LENGTH: 917 amino acids
330         (B) TYPE: amino acid
331         (D) TOPOLOGY: linear

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/025,524

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Input Set : A:\EP.txt

Output Set: N:\CRF3\07242002\J025524.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:2058 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27
L:2258 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=29
L:2274 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=30
L:2302 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=32
L:2386 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=34
L:2400 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=35
L:2414 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=36
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L:2470 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=40
L:2484 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=41
L:2498 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=42